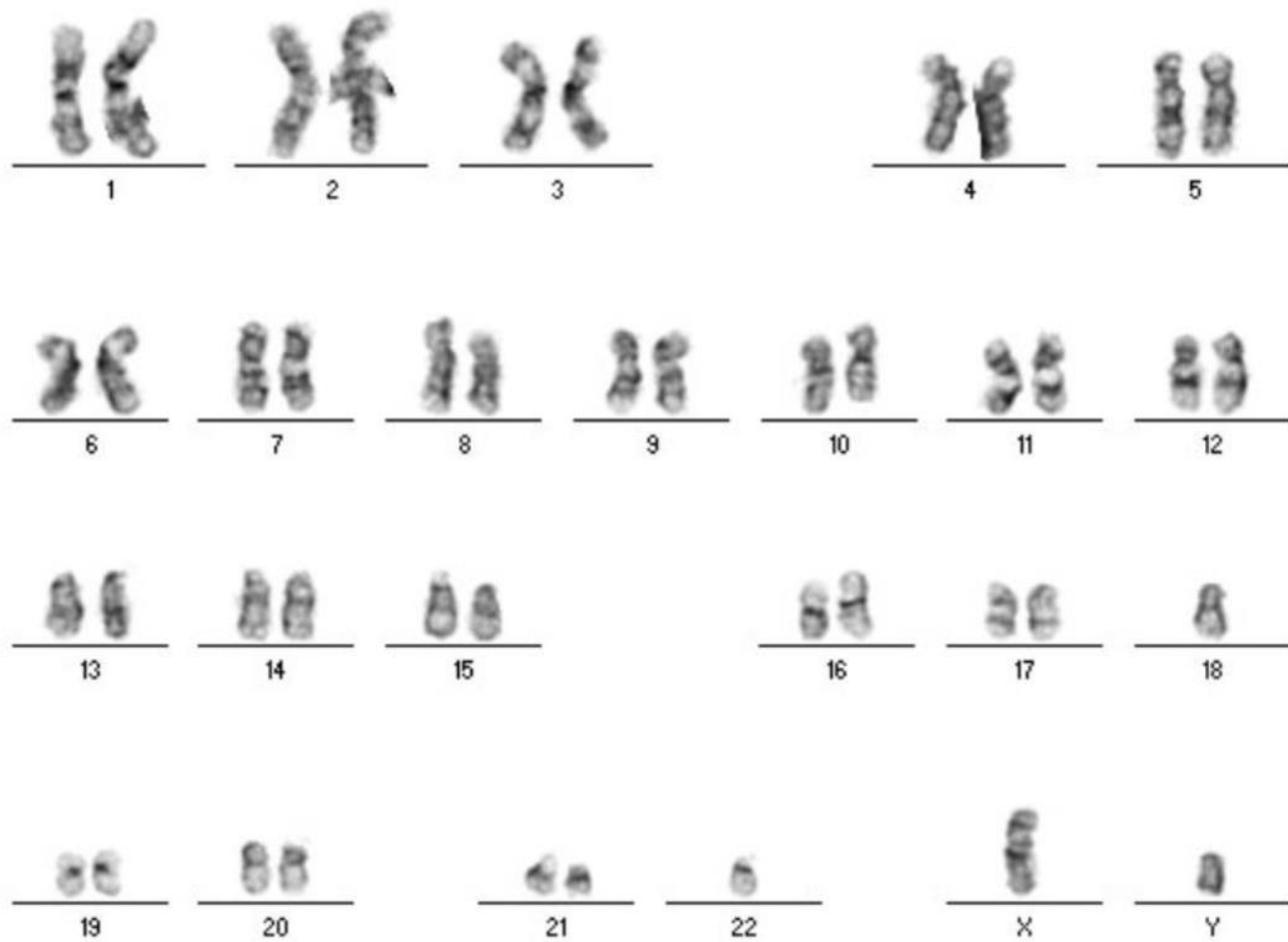
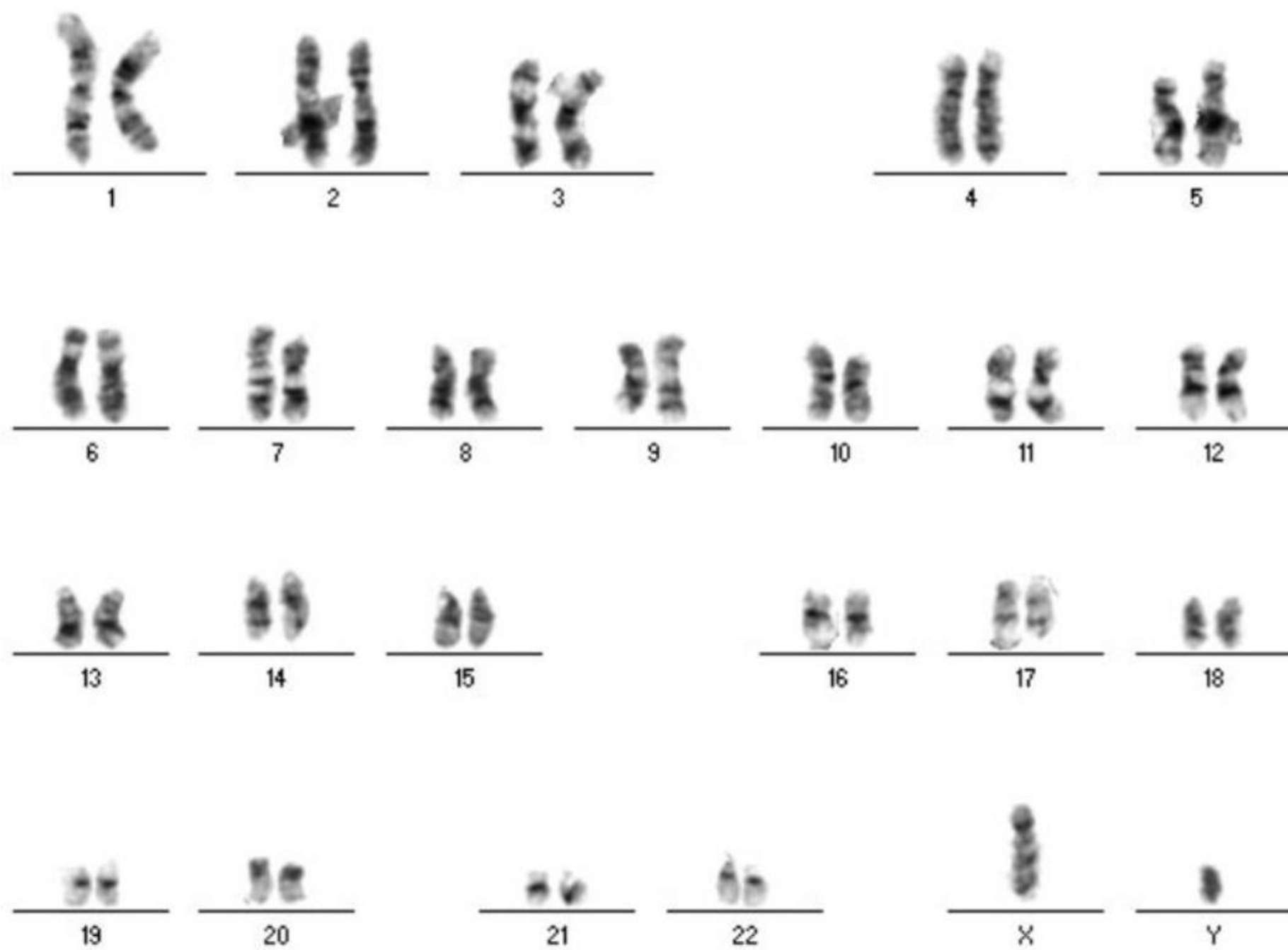
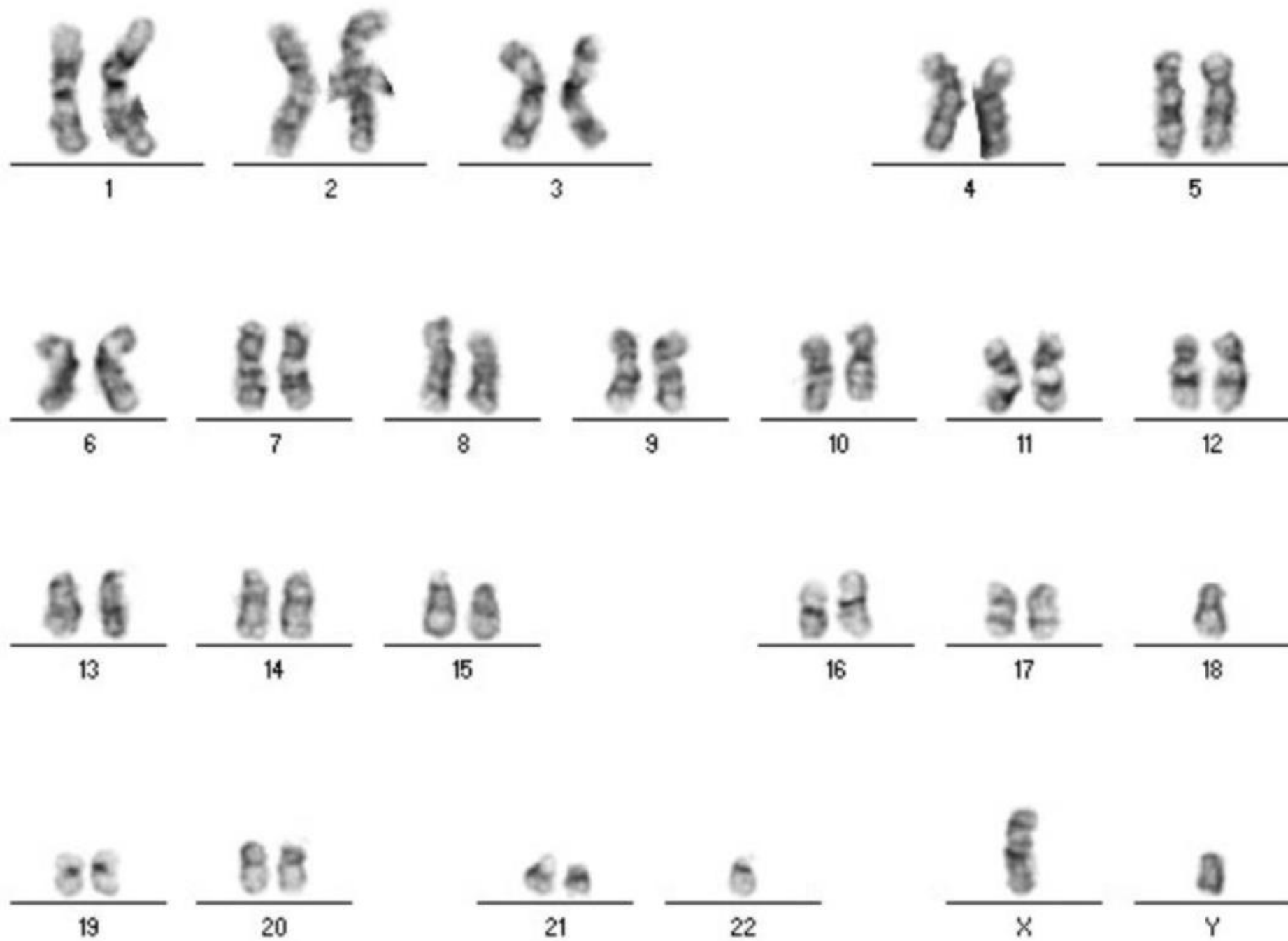
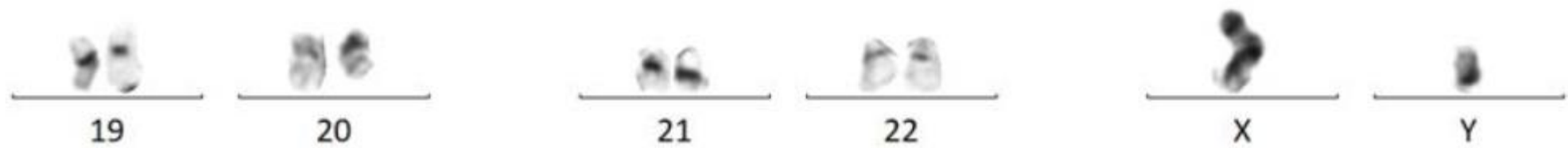
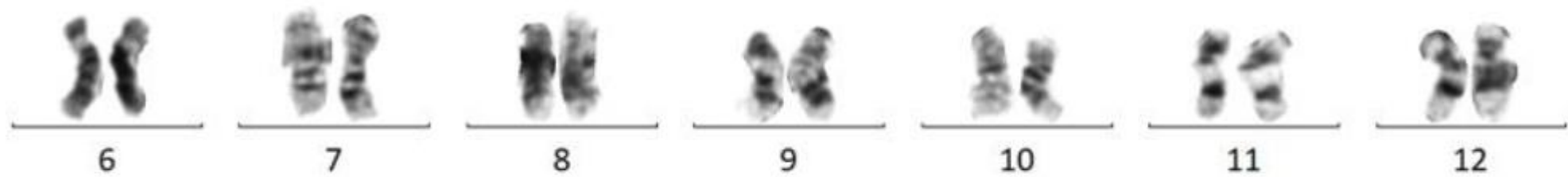
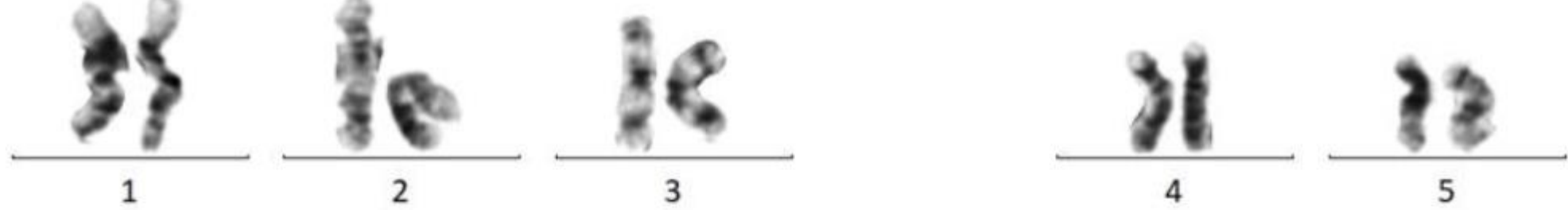


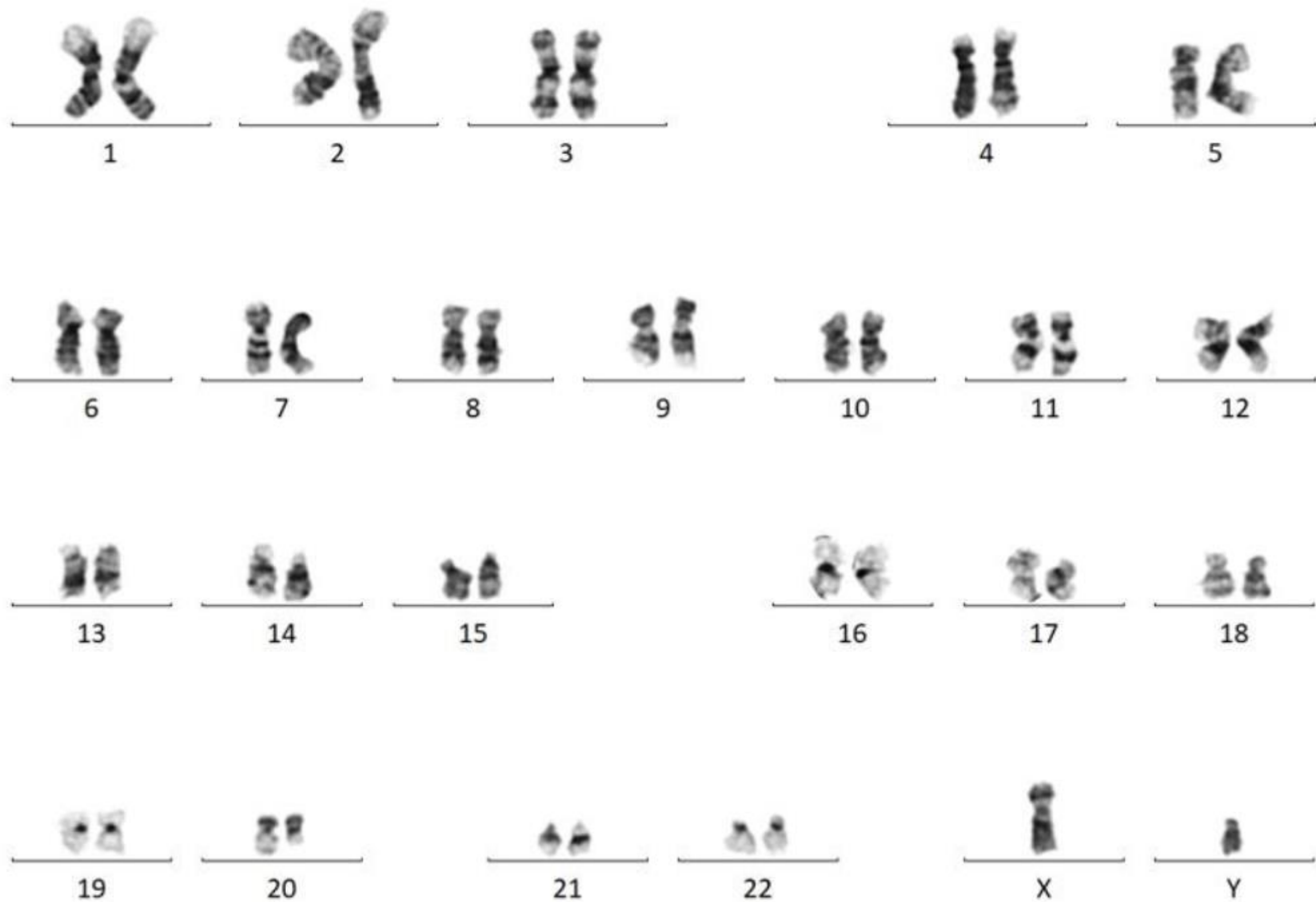
- You are to provide the ISCN nomenclature of the patient based on the karyotype given for selected metaphases. Consider that the remaining metaphases have a normal karyotype with the corresponding sex chromosomes. 20 metaphases have been analyzed in total.
- You are to determine if the variant identified is a reportable variant based on sequencing reads and quality metrics.
- You are to provide coding and protein nomenclature for the variant highlighted by the red arrow.
- You are to determine which variants are to be reported using the AMP/ASCO/CAP somatic variant classification scheme.
- Variant allele frequency of each candidate variant is to be noted on the report.
- Where applicable, suspicious germline variant(s) for germline sequencing should be identified.

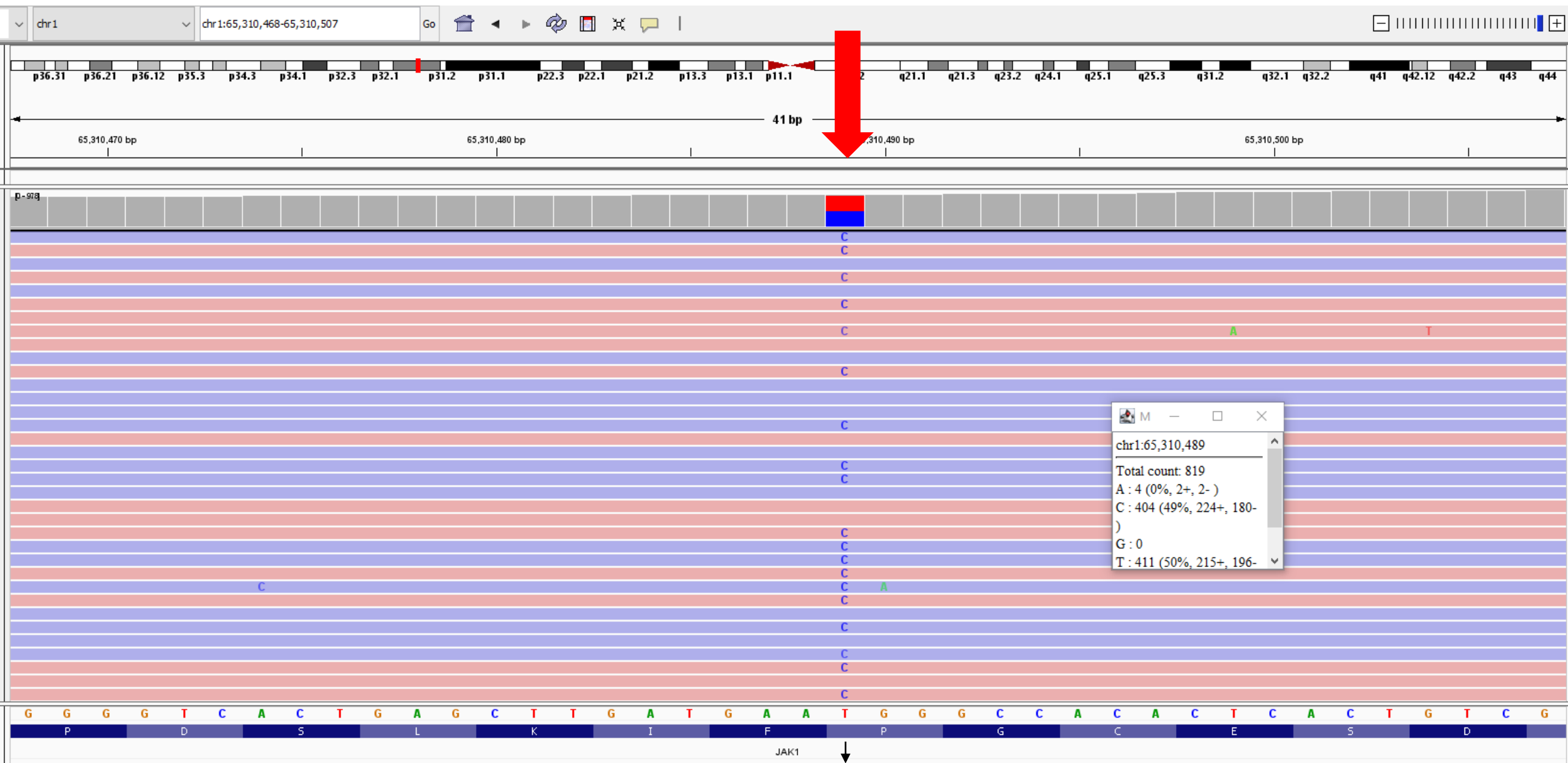






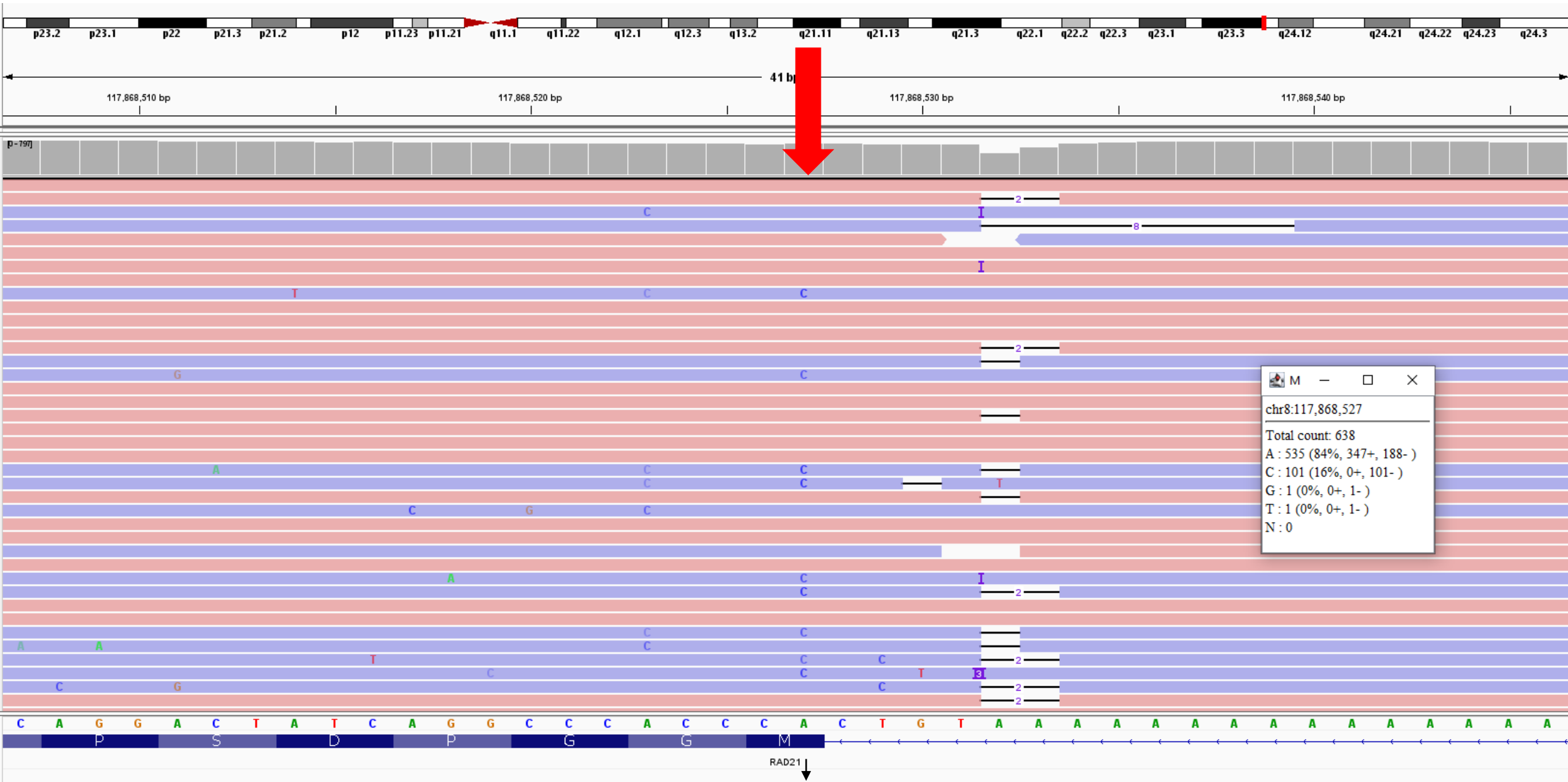






- strand

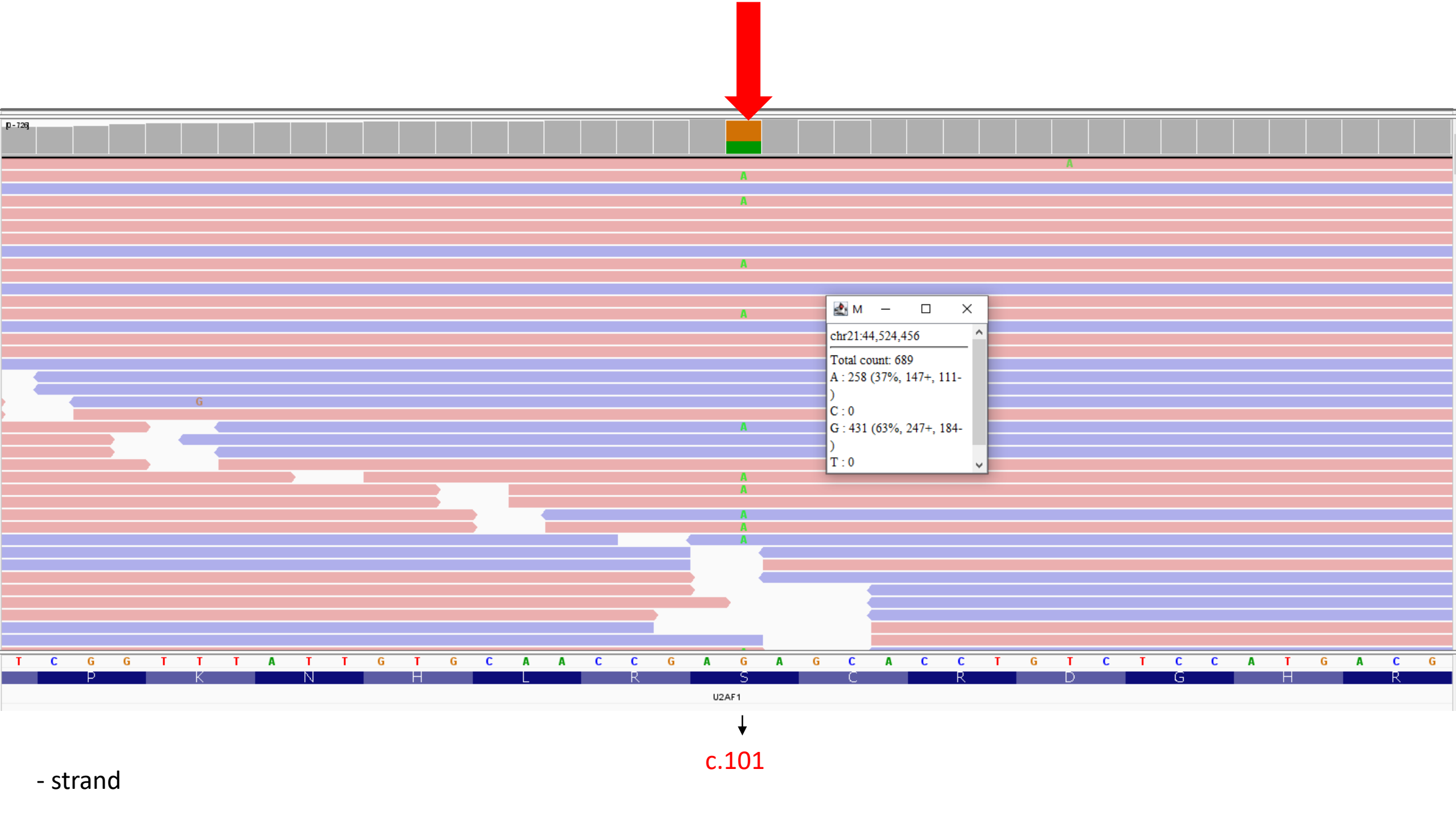
c.2199

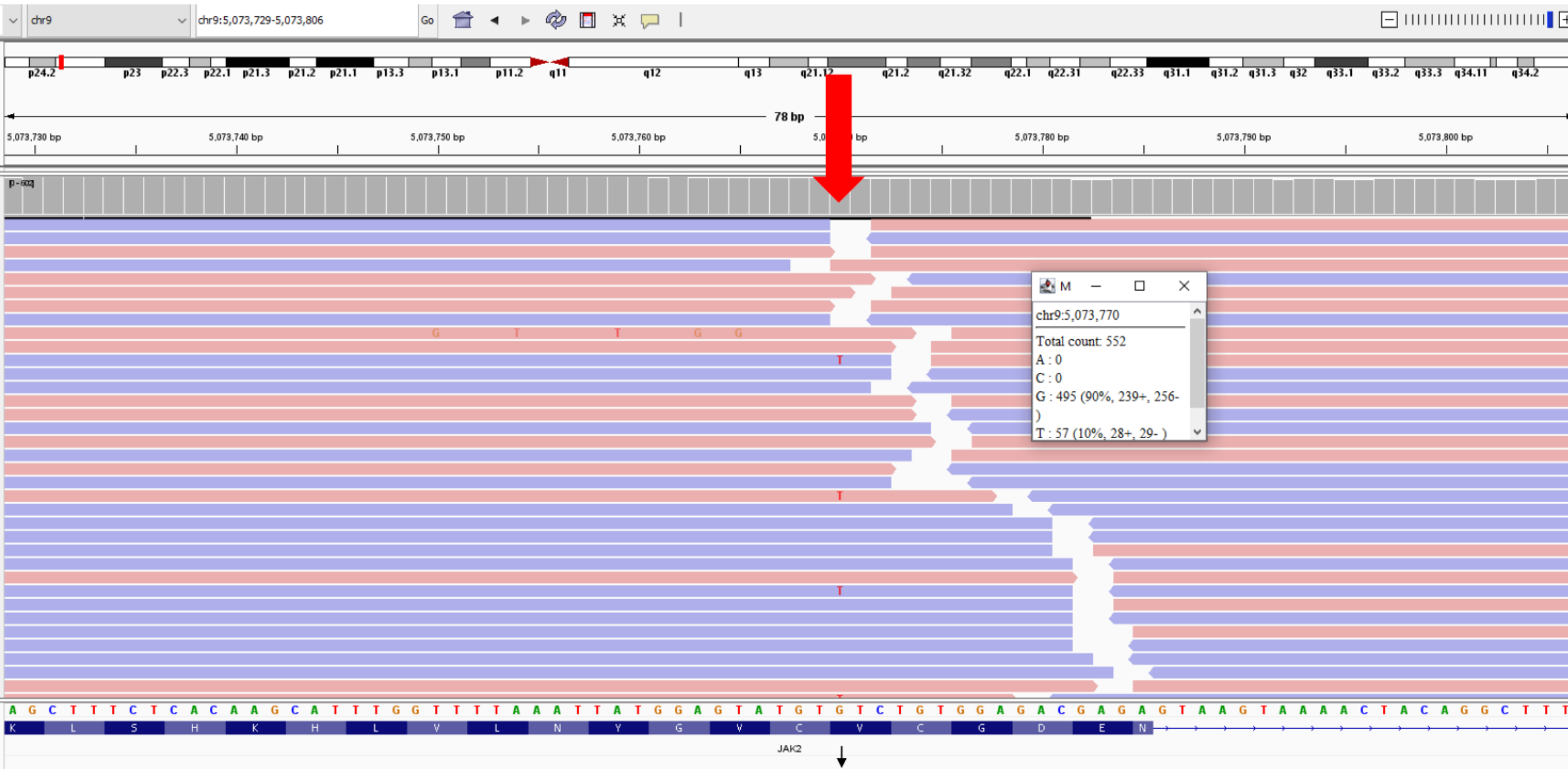


- strand

c.815







+ strand

c.1849